

FIG. 1

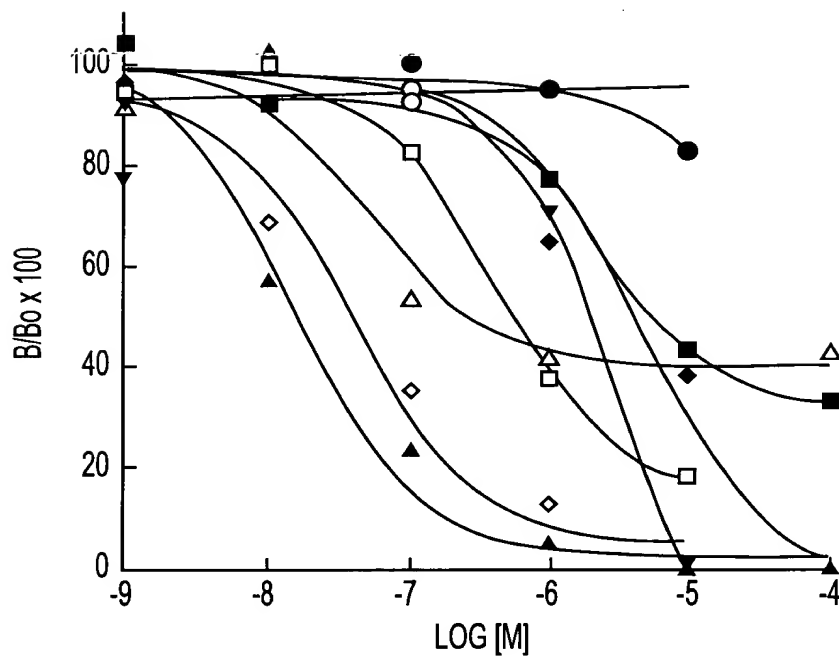


FIG. 2

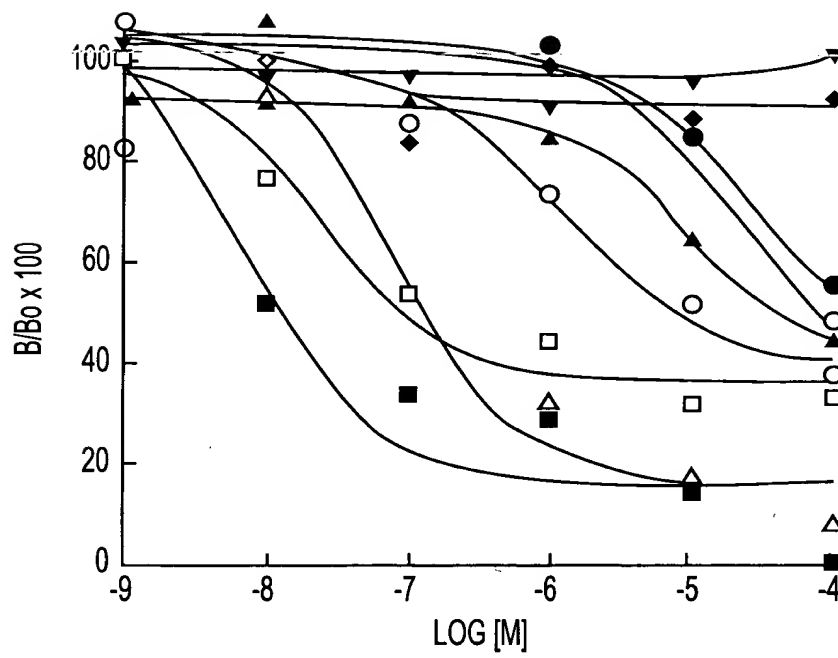


FIG. 3

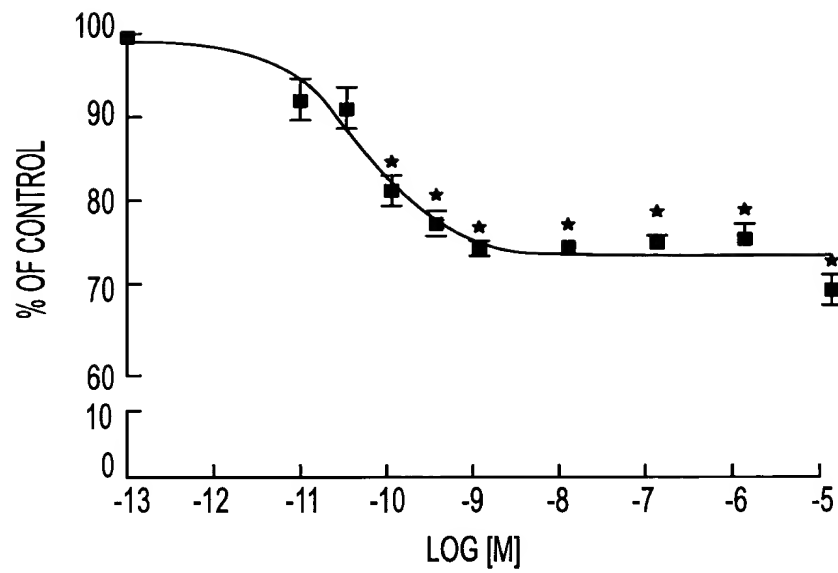


FIG. 4

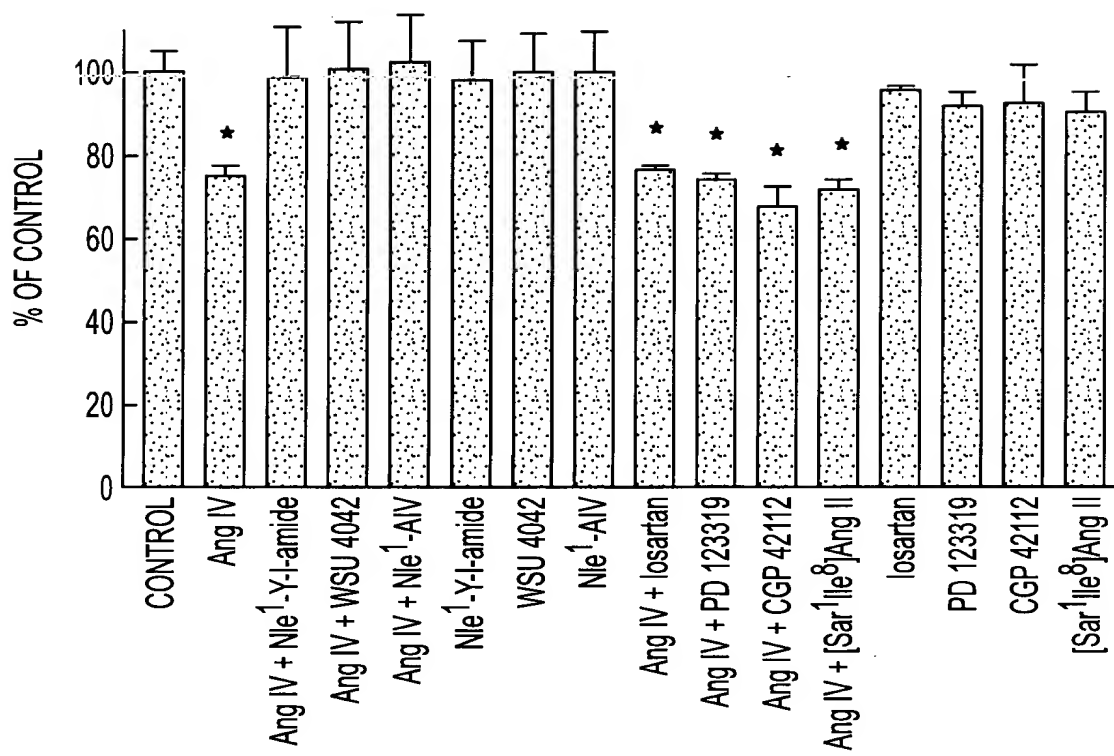


FIG. 5

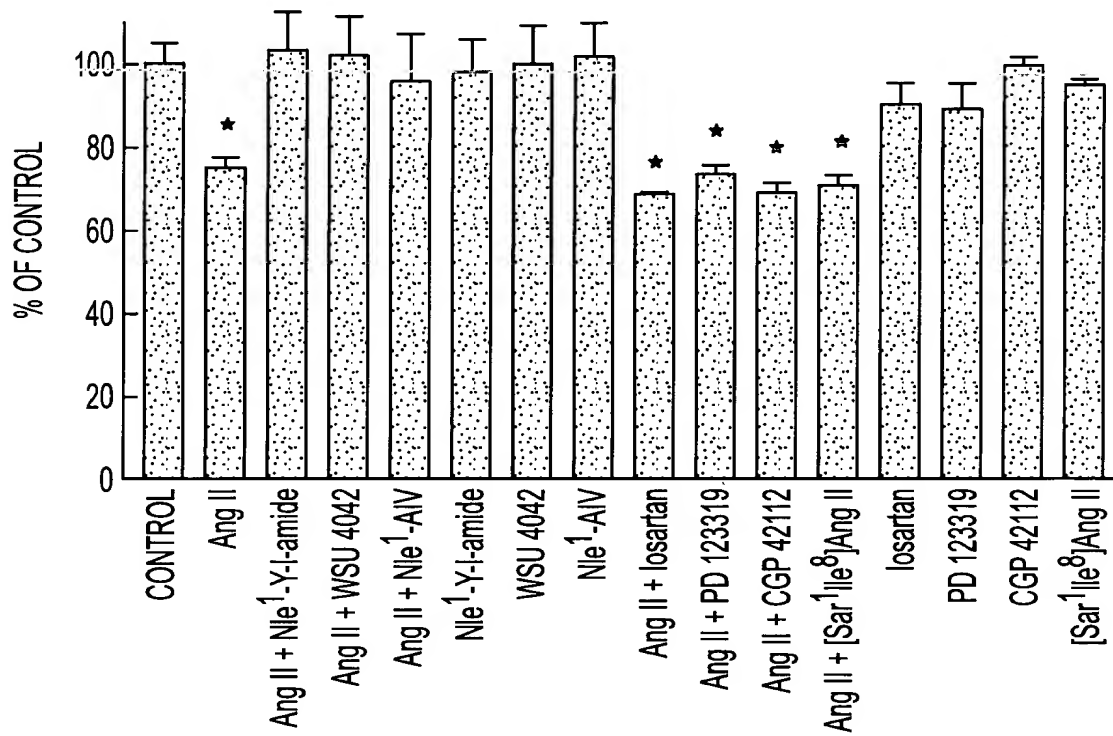


FIG. 6

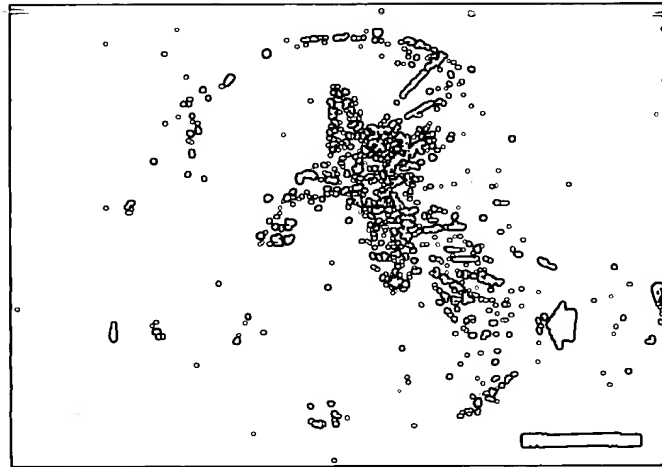


FIG. 7

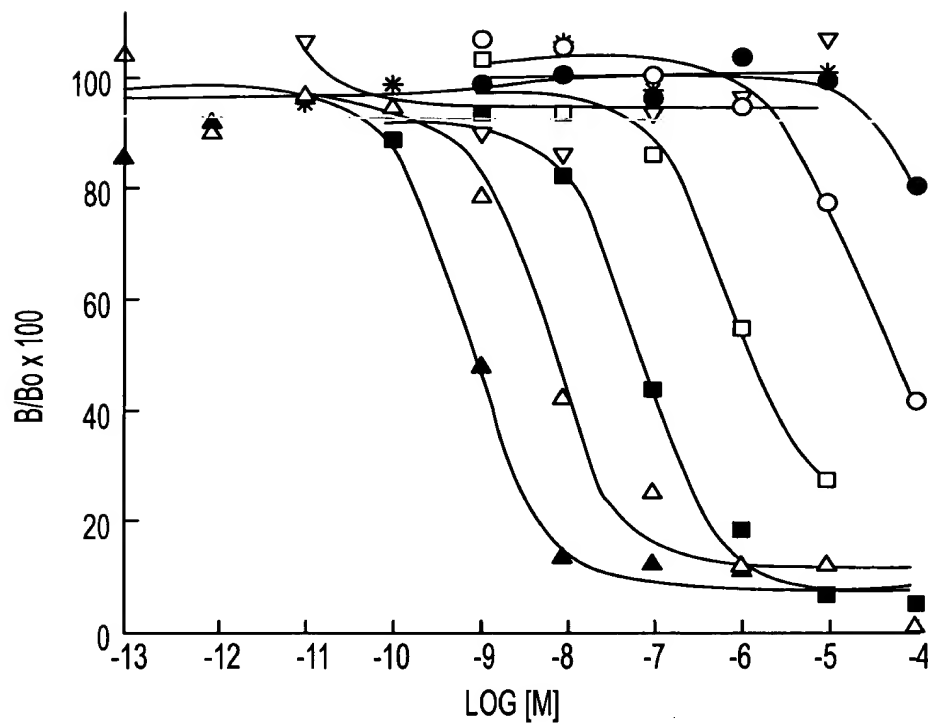


FIG. 8

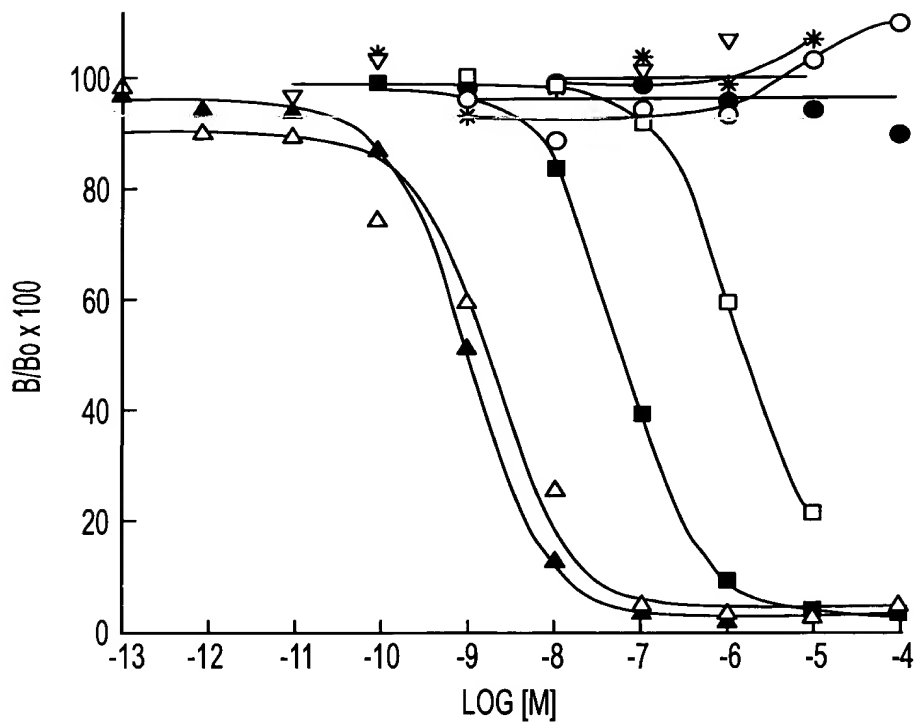


FIG. 9

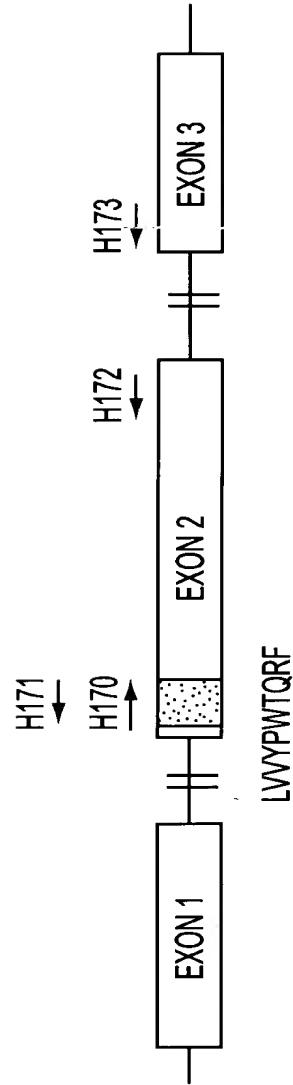


FIG. 10A

OLIGONUCLEOTIDE SEQUENCES:

H170: 5' CTGGTTGCTACCCCTGGACTCAGAG 3'
 H171: 5' CTCAGTCCAGGGGTAGACAACAG 3'
 H172: 5' CTCAGGATCCACATGCAGCTTATCAGAG 3'
 H173: 5' CAGCACCACTAGCACATTGCC 3'

FIG. 10B

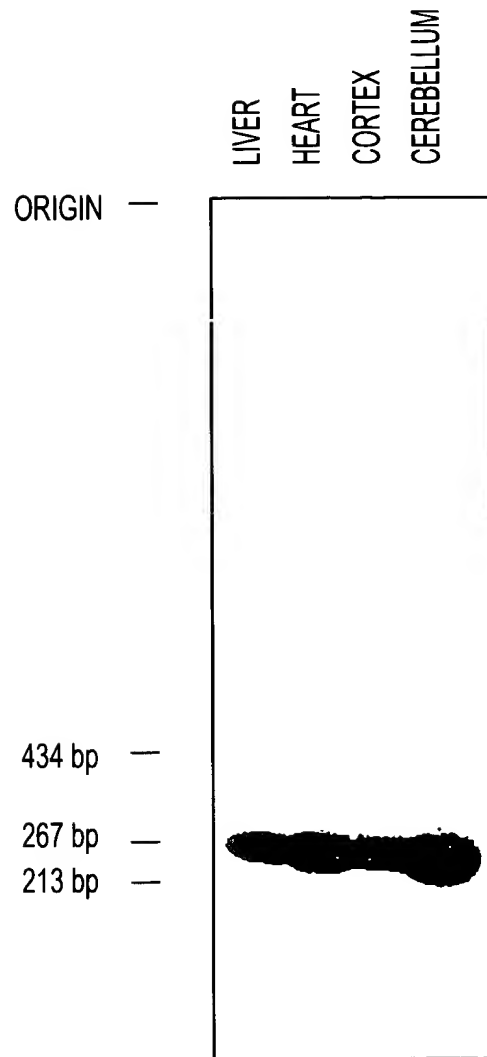


FIG. 11

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                                10      20      30
EX      CACAAACTCAGAAACAGACACCATGGTGCACCTGA
RNBGLO  TGCTTCTGACATAGTTGTGTTGACTCACAAACTCAGAAACAGACACCATGGTGCACCTGA
                                10      20      30      40      50      60
                                40      50      60      70      80      90
EX      CTGATGCTGAGAAGGCTGCTGTTAATGGCCTGTGGGGAAAGGTGAACCCTGATGATGTTG
RNBGLO  CTGATGCTGAGAAGGCTGCTGTTAATGGCCTGTGGGGAAAGGTGAACCCTGATGATGTTG
                                70      80      90      100     110     120
                                100     110     120     130     140     150
EX      GTGGCGAGGCCCTGGGCAGGCTGCTGGTTGTCTACCCTTGGACCCAGAGGTACTTTGATA
RNBGLO  GTGGCGAGGCCCTGGGCAGGCTGCTGGTTGTCTACCCTTGGACCCAGAGGTACTTTGATA
                                130     140     150     160     170     180
                                160     170     180     190     200     210
EX      GCTTTGGGGACCTGTCCTCTGCCTCTGCTATCATGGGTAACCCTAAGGTGAAGGGCCATG
RNBGLO  GCTTTGGGGACCTGTCCTCTGCCTCTGCTATCATGGGTAACCCTAAGGTGAAGGGCCATG
                                190     200     210     220     230     240
                                220     230     240     250     260     270
EX      GCAAGAAGGTGATAAACGCCTTCAATGATGGCCTGAAACACTTGGACAACCTCAAGGGCA
RNBGLO  GCAAGAAGGTGATAAACGCCTTCAATGATGGCCTGAAACACTTGGACAACCTCAAGGGCA
                                250     260     270     280     290     300
                                280     290     300     310     320     330
EX      CCTTTGCTCATCTGAGTGAAGTCCACTGTGACAAGCTGCATGTGGATCCTGAGAACTTCA
RNBGLO  CCTTTGCTCATCTGAGTGAAGTCCACTGTGACAAGCTGCATGTGGATCCTGAGAACTTCA
                                310     320     330     340     350     360
                                340     350     360     370     380     390
EX      GGCTCCTGGGCAATATGATTGTGATTGTGTTGGGCCACCACCTGGGCAAGGAATTCACCC
RNBGLO  GGCTCCTGGGCAATATGATTGTGATTGTGTTGGGCCACCACCTGGGCAAGGAATTCACCC
                                370     380     390     400     410     420
                                400     410     420     430     440     450
EX      CCTGTGCACAGGCTGCCTTCCAGAAGGTGGTGGCTGGAGTGGCCAGTGCCCTGGCTCACA
RNBGLO  CCTGTGCACAGGCTGCCTTCCAGAAGGTGGTGGCTGGAGTGGCCAGTGCCCTGGCTCACA
                                430     440     450     460     470     480
                                460     470     480     490     500     510
EX      AGTACCACTAAACCTCTTTTCCTGCTCTTGTCTTTGTGCAATGGTCAATTGTTCCCAAGA
RNBGLO  AGTACCACTAAACCTCTTTTCCTGCTCTTGTCTTTGTGCAATGGTCAATTGTTCCCAAGA
                                490     500     510     520     530     540
                                520     530     540     550     560     570
EX      GAGCATCTGTCAGTTGTTGTCAAAATGACAAAGACCTTTGAAAATCTGTCCTACTAATAA
RNBGLO  GAGCATCTGTCAGTTGTTGTCAAAATGACAAAGACCTTTGAAAATCTGTCCTACTAATAA
                                580     590     600     610
EX      AAGGCATTTACTTTCACTGCAAAAAAAAAAAAAAAAAAAAA
RNBGLO  AAGGCATTTACTTTCACTGC
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FIG. 12

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                                10      20      30
EX      CACAAACTCAGAAACAGACACCATGGTGCACCTGA
                                M V H L

      40      50      60      70      80      90
EX CTGATGCTGAGAAGGCTGCTGTTAATGGCCTGTGGGGAAAGGTGAACCCTGATGATGTTG
  T D A E K A A V N G L W G K V N P D D V

      100     110     120     130     140     150
EX GTGGCGAGGCCCTGGGCAGGCTGCTGGTTGTCTACCCTTGACCCAGAGGTACTTTGATA
  G G E A L G R L L V V Y P W T Q R Y F D

      160     170     180     190     200     210
EX GCTTTGGGGACCTGTCCTCTGCCTCTGCTATCATGGGTAACCCTAAGGTGAAGGCCCATG
  S F G D L S S A S A I M G N P K V K A H

      220     230     240     250     260     270
EX GCAAGAAGGTGATAAACGCCCTTCAATGATGGCCTGAAACACTTGGACAACCTCAAGGGCA
  G K K V I N A F N D G L K H L D N L K G

      280     290     300     310     320     330
EX CCTTTGCTCATCTGAGTGAAGTCCACTGTGACAAGCTGCATGTGGATCCTGAGAACTTCA
  T F A H L S E L H C D K L H V D P E N F

      340     350     360     370     380     390
EX GGCTCCTGGGCAATATGATTGTGATTGTGTTGGGCCACCACTGGGCAAGGAATTCACCC
  R L L G N M I V I V L G H H L G K E F T

      400     410     420     430     440     450
EX CCTGTGCACAGGCTGCCTTCCAGAAGGTGGTGGCTGGAGTGGCCAGTGGCCTGGCTCACA
  P C A Q A A F Q K V V A G V A S A L A H

      460     470     480     490     500     510
EX AGTACCACTAAACCTCTTTTCCTGCTCTTGTCTTTGTGCAATGGTCAATTGTTCCCAAGA
  K Y H *

      520     530     540     550     560     570
EX GAGCATCTGTCAGTTGTTGTCAAAATGACAAAGACCTTTGAAAATCTGTCCTACTAATAA

      580     590     600     610
EX AAGGCATTTACTTTCACTGCAAAAAAAAAAAAAAAAAA
```

FIG. 13

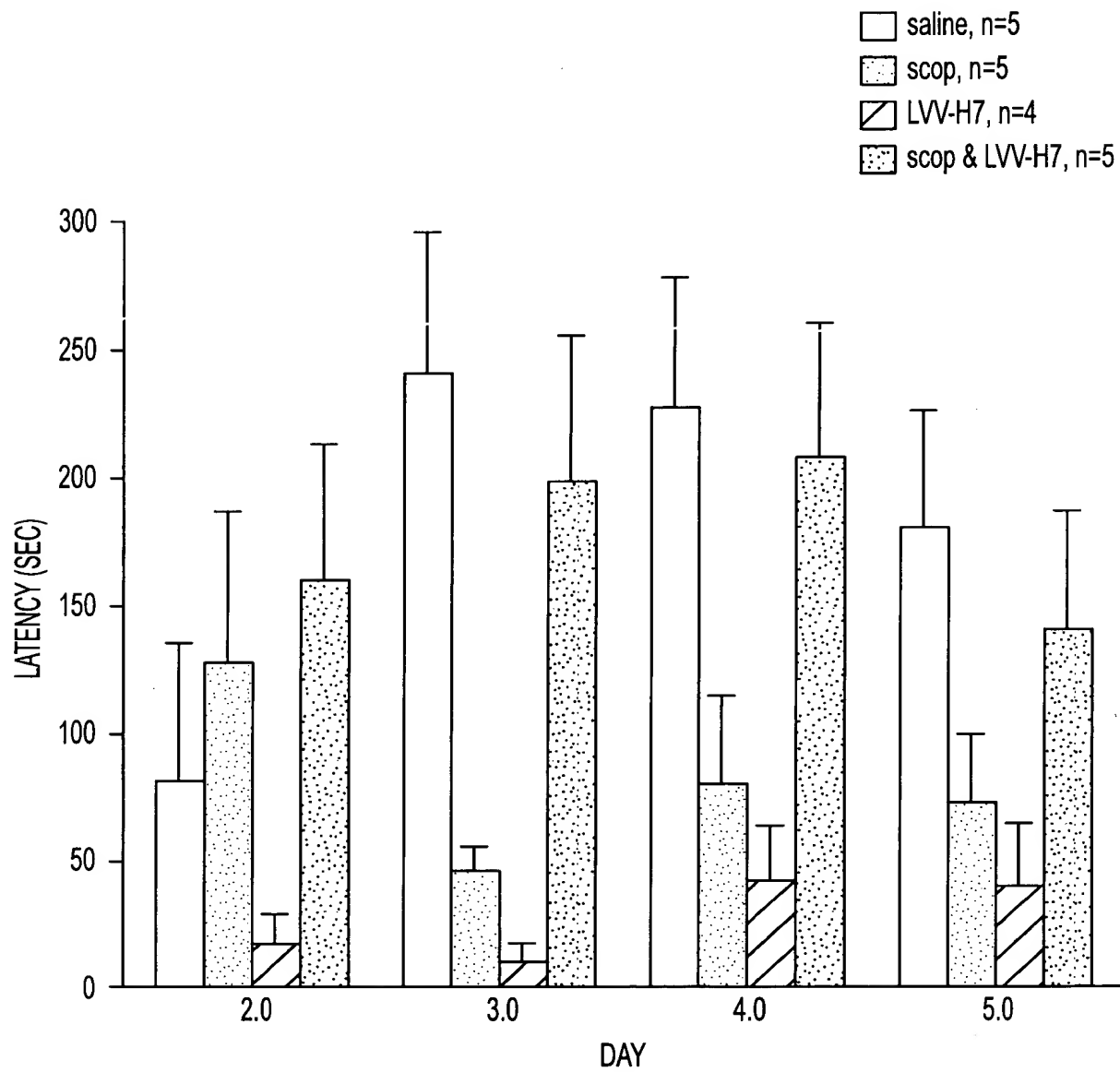


FIG. 14

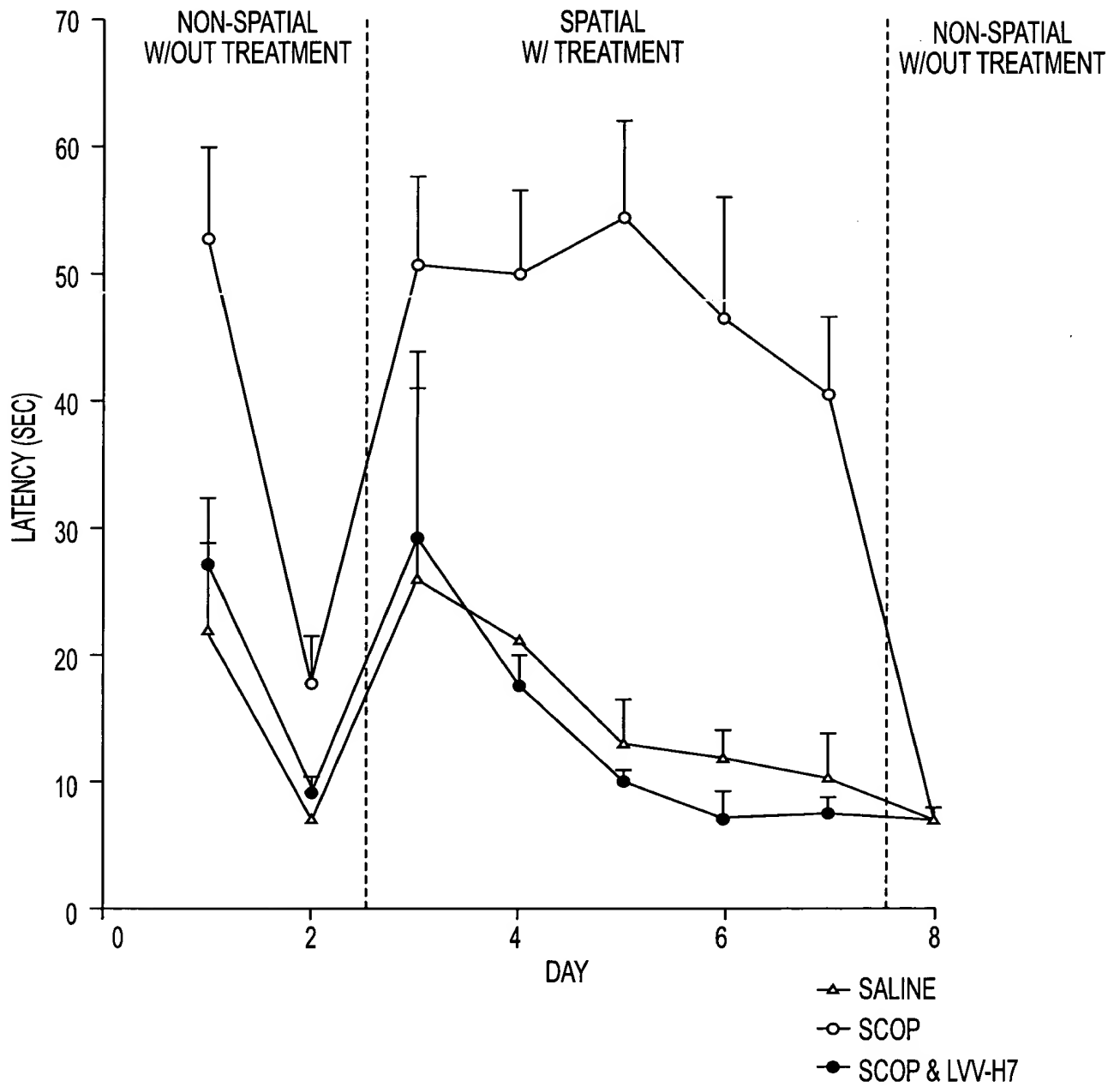


FIG. 15